

Untitled

Title: US-10-574-297-34
 Perfect score: 5178
 Sequence: 1 MYLDRFRQCPSSLQI PRSAW.....AAGDRI NI PWSFHAGYRYSF 1010

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

RESULT 2

ABU22871

ID ABU22871 standard; protein; 998 AA.

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AC ABU22871;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #8398.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Bordetella pertussis.

XX

PN WD200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WD-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR

06-SEP-2001; 2001US-00948993.

PR

25-OCT-2001; 2001US-0342923P.

PR

08-FEB-2002; 2002US-00072851.

PR

06-MAR-2002; 2002US-0362699P.

XX

PA (ELI T.) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW

PI

Wail D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HT;

XX

DR VPI; 2003-029926/02.

DR

N-PSDB; ACA26741.

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PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

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PS Claim 25; SEQ ID NO 50795; 1766pp; English.

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CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:

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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WPO at ftp.wpo.int/pub/published_pct_sequences

XX
SQ Sequence 998 AA;

Query Match 98.7% Score 5109; DB 6; Length 998;
Best Local Similarity 99.9% Pred. No. 3.3e-295;
Matches 997; Conservative 1; Msmatches 0; Indels 0; Gaps 0;

Qy	13	LQI PRSAWRLHALAAALALAGMARLAPAAQAQPPVAGAPHACDAGCEGFDRHNTLI	72
Db	1	MQ PRSAWRLHALAAALALAGMARLAPAAQAQPPVAGAPHACDAGCEGFDRHNTLI	60
Qy	73	AVFDDGVGI NDDDPDELGETAPPTLKDI HI SVEHKNPMSKPAI GVRVSGACRALTAGS	132
Db	61	AVFDDGVGI NDDDPDELGETAPPTLKDI HI SVEHKNPMSKPAI GVRVSGACRALTAGS	120
Qy	133	TI DATEGGI PAVVRGGTLELDGVTVAGGEGMEPMIVSDAGSRLSVRGGVLGGEAPGVGL	192
Db	121	TI DATEGGI PAVVRGGTLELDGVTVAGGEGMEPMIVSDAGSRLSVRGGVLGGEAPGVGL	180
Qy	193	VRAAQGGQASI I DATLQSI LGPALI ADGGSI SVAGSSI DIMDMPGFPPPPPLPGAPLAA	252
Db	181	VRAAQGGQASI I DATLQSI LGPALI ADGGSI SVAGSSI DIMDMPGFPPPPPLPGAPLAA	240
Qy	253	HPPLDRVAAVHAGDQGVTLREVALRAHGPOATGYAYMPGSEI TLQGGTIVSVCDDGAG	312
Db	241	HPPLDRVAAVHAGDQGVTLREVALRAHGPOATGYAYMPGSEI TLQGGTIVSVCDDGAG	300
Qy	313	WVAGAGLLDALPPGGTVRLDGITVSTDGANTDAVLVRGDAARAEVNTVLRRTAKSLAAGV	372
Db	301	WVAGAGLLDALPPGGTVRLDGITVSTDGANTDAVLVRGDAARAEVNTVLRRTAKSLAAGV	360
Qy	373	SAGHGRVTLRQTRI ETAGAGAEGI SVLGFEPQSGSGPASVDMQGGSI TTTGNFAAGI AL	432
Db	361	SAGHGRVTLRQTRI ETAGAGAEGI SVLGFEPQSGSGPASVDMQGGSI TTTGNFAAGI AL	420

Untitled

Qy 433 THGSARLEGVAVRAEGSGSSAAQLANGTLVWSAGSLASAGSGAI SVTDTPCLKLMPGALAS 492
 Db 421 THGSARLEGVAVRAEGSGSSAAQLANGTLVWSAGSLASAGSGAI SVTDTPCLKLMPGALAS 480
 Qy 493 STVSVRLTDGATACGGNGVFLQQHSTI PVAVALESGLARIGDI VADGNKPLDAGI SL.SVA 552
 Db 481 STVSVRLTDGATACGGNGVFLQQHSTI PVAVALESGLARIGDI VADGNKPLDAGI SL.SVA 540
 Qy 553 SGAAMHGATQMLQSATLGKGGTWMVNADSRVQDMSMRGGRVFQAPAPEASYKTLTLQTL 612
 Db 541 SGAAMHGATQMLQSATLGKGGTWMVNADSRVQDMSMRGGRVFQAPAPEASYKTLTLQTL 600
 Qy 613 DGNQVFLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTGCGGNAT 672
 Db 601 DGNQVFLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTGCGGNAT 660
 Qy 673 FRLANVGKAVDLGTWRYSLAEDPKTHVWBLQRAGQALSGAANAAVNAADLSSI ALAESNA 732
 Db 661 FRLANVGKAVDLGTWRYSLAEDPKTHVWBLQRAGQALSGAANAAVNAADLSSI ALAESNA 720
 Qy 733 LDKRLGELRLRADAGFPWARTFSERCQI SNRHARAYDQTVSGLIEI GLDRGMSASGGRWYA 792
 Db 721 LDKRLGELRLRADAGFPWARTFSERCQI SNRHARAYDQTVSGLIEI GLDRGMSASGGRWYA 780
 Qy 793 GGLLGTYADRTYPGDGGKVKGLHVGGYAAVYVDGGYYLDTVLRLGRYDQQYNI AGTDG 852
 Db 781 GGLLGTYADRTYPGDGGKVKGLHVGGYAAVYVDGGYYLDTVLRLGRYDQQYNI AGTDG 840
 Qy 853 GRVTADYRTSGAAWSLEGGRRFELPNDFWAEPOAEVMLWRTSGKRYRASNGLRVKVDANT 912
 Db 841 GRVTADYRTSGAAWSLEGGRRFELPNDFWAEPOAEVMLWRTSGKRYRASNGLRVKVDANT 900
 Qy 913 ATLGRLLGRFGRRI ALAGGNI VQPYARLGATGCEFKSTGDVRTNGI GHAGAGRHGRVELGA 972
 Db 901 ATLGRLLGRFGRRI ALAGGNI VQPYARLGATGCEFKSTGDVRTNGI GHAGAGRHGRVELGA 960
 Qy 973 GVDAAALGKGHNLVASYEYAAGDRI NI PWSFHAGYRYSF 1010
 Db 961 GVDAAALGKGHNLVASYEYAAGDRI NI PWSFHAGYRYSF 998